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RAW SEQUENCE LISTING

DATE: 11/09/2000

PATENT APPLICATION: US/09/695,451

TIME: 11:54:56

Input Set : A:\PTO.txt

Output Set: N:\CRF3\11092000\I695451.raw

ENTERED

3 <110> APPLICANT: Brenda F. Baker
 4 Lex M. Cowsert
 5 Hong Zhang
 6 Nicholas M. Dean
 8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1 EXPRESSION
 10 <130> FILE REFERENCE: ISPH-0518
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/695,451
 C--> 12 <141> CURRENT FILING DATE: 2000-10-24
 12 <150> PRIOR APPLICATION NUMBER: US 09/106,038
 13 <151> PRIOR FILING DATE: 1998-06-26
 15 <150> PRIOR APPLICATION NUMBER: PCT/US99/13763
 16 <151> PRIOR FILING DATE: 1999-06-17
 18 <160> NUMBER OF SEQ ID NOS: 246
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2161
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (256)...(1623)
 31 <400> SEQUENCE: 1
 32 cggcccagtg atcttgaacc ccaaaggcca gaactggagc ctccagtcag agaattctga 60
 33 gaaaattaaa gcagagagga ggggagagat cactgggacc aggccgtgat ctctatgccc 120
 34 gagtctcaac cctcaactgt caccocaagg cacttgggac gtccctggaca gaccgagtc 180
 35 cgggaagccc cagcactgcc gctgccacac tgccctgagc ccaaatgggg gagtgaaggg 240
 36 ccatagtgtg ctggc atg ggc ctc tcc acc gtg cct gac ctg ctg ctg ccg 291
 37 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro
 38 1 5 10
 40 ctg gtg ctc ctg gag ctg ttg gtg gga ata tac ccc tca ggg gtt att 339
 41 Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile
 42 15 20 25
 44 gga ctg gtc cct cac cta ggg gac agg gag aag aga gat agt gtg tgt 387
 45 Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys
 46 30 35 40
 48 ccc caa gga aaa tat atc cac cct caa aat aat tgg att tgc tgt acc 435
 49 Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
 50 45 50 55 60
 52 aag tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg 483
 53 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly
 54 65 70 75
 56 cag gat acg gac tgc agg gag tgt gag agc ggc tcc ttc acc gct tca 531
 57 Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser
 58 80 85 90
 60 gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa 579
 61 Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu
 62 95 100 105

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64  atg ggt cag gtg gag atc tct tct tgc aca gtg gac cgg gac acc gtg 627
65  Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val
66      110                      115                      120
68  tgt ggc tgc agg aag aac cag tac cgg cat tat tgg agt gaa aac ctt 675
69  Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu
70      125                      130                      135                      140
72  ttc caq tgc ttc aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc 723
73  Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu
74      145                      150                      155
76  tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc 771
77  Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe
78      160                      165                      170
80  ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc 819
81  Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser
82      175                      180                      185
84  ctg gag tgc acg aag ttg tgc cta ccc cag att gag aat gtt aag ggc 867
85  Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly
86      190                      195                      200
88  act gag gac tca ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt 915
89  Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe
90      205                      210                      215                      220
92  ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt tta atg tat cgc tac 963
93  Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr
94      225                      230                      235
96  caa cgg tgg aag tcc aag ctc tac tcc att gtt tgt ggg aaa tcc aca 1011
97  Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr
98      240                      245                      250
100 cct gaa aaa gag ggg gag ctt gaa gga act act act aag ccc ctg gcc 1059
101  Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala
102      255                      260                      265
104 cca aac cca agc ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc 1107
105  Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly
106      270                      275                      280
108 ttc agt ccc gtg ccc agt tcc acc ttc acc tcc agc tcc acc tat acc 1155
109  Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
110      285                      290                      295                      300
112 ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca 1203
113  Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro
114      305                      310                      315
116 ccc tat cag ggg gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac 1251
117  Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp
118      320                      325                      330
120 ccc atc ccc aac ccc ctt cag aag tgg gag gac agc gcc cac aag cca 1299
121  Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro
122      335                      340                      345
124 cag agc cta gac act gat gac ccc gcg acg ctg tac gcc gtg gtg gag 1347
125  Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu
126      350                      355                      360
128 aac gtg ccc ccg ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg 1395

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```

129   Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu
130   365                               370                               375                               380
132   agc gac cac gag atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg   1443
133   Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu
134   385                               390                               395
136   cgc gag gcg caa tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg   1491
137   Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro
138   400                               405                               410
140   cgg cgc gag gcc acg ctg gag ctg ctg gga cgc gty ctc cgc gac atg   1539
141   Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met
142   415                               420                               425
144   gac ctg ctg ggc tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc   1587
145   Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro
146   430                               435                               440
148   gcc gcc ctc ccg ccc gcg ccc agt ctt ctc aga tga ggctgcgccc   1633
149   Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg *
150   445                               450                               455
152   ctgcgggcag ctctaaggac cgtcctgcga gatcgccctc caaccccact tttttctgga 1693
153   aaggaggggt cctgcagggg caagcaggag ctacgagcgc ctaacttggg gctaaccctt 1753
154   cgatgtacat agcttttctc agctgcctgc gcgccgccga cagtcagcgc tgtgcgcgcg 1813
155   gagagagggt cgcggtgggc tcaagagcct gagtgggtgg ttgcgagga tgagggagcg 1873
156   tatgcctcat gccggttttg ggtgtcctca ccagcaaggc tgcgcggggg cccctgggtc 1933
157   gtccctgagc ctttttcaca gtgcataaag agtttttttt gtttttggtt tgttttgttt 1993
158   tgtttttaaa tcaatcatgt tactaataa gaaacttggc actcctgtgc cctctgcctg 2053
159   gacaagcaca tagcaagctg aactgtccta aggcaggggc gagcacggaa caatggggcc 2113
160   ttcagctgga gctgtggact ttgtacata cactaaaatt ctgaagtt   2161
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 23
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: PCR Primer
170 <400> SEQUENCE: 2
171   gcttcagaaa accacctcag aca   23
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 19
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: PCR Primer
181 <400> SEQUENCE: 3
182   ccggtccact gtgcaagaa   19
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 24
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: PCR Probe
192 <400> SEQUENCE: 4

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Input Set : A:\PTO.txt

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```

193   tcagctgctc caaatgccga aagg                24
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 19
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: PCR Primer
203 <400> SEQUENCE: 5
204   gaaggtgaag gtcggagtc                19
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: PCR Primer
214 <400> SEQUENCE: 6
215   gaagatggtg atgggatttc                20
217 <210> SEQ ID NO: 7
218 <211> LENGTH: 20
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: PCR Probe
225 <400> SEQUENCE: 7
226   caagcttccc gttctcagcc                20
228 <210> SEQ ID NO: 8
229 <211> LENGTH: 18
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Antisense Oligonucleotide
236 <400> SEQUENCE: 8
237   ttctctggac tgaggctc                18
239 <210> SEQ ID NO: 9
240 <211> LENGTH: 18
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Antisense Oligonucleotide
247 <400> SEQUENCE: 9
248   tccccctctc tctgcttt                18
250 <210> SEQ ID NO: 10
251 <211> LENGTH: 18
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Antisense Oligonucleotide
258 <400> SEQUENCE: 10
259   agactcgggc atagagat                18

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 PATENT APPLICATION: US/09/695,451 TIME: 11:54:56 .

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\11092000\I695451.raw

```

261 <210> SEQ ID NO: 11
262 <211> LENGTH: 18
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Antisense Oligonucleotide
269 <400> SEQUENCE: 11
270   gggtgagact cgggcata                               18
272 <210> SEQ ID NO: 12
273 <211> LENGTH: 18
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Antisense Oligonucleotide
280 <400> SEQUENCE: 12
281   tgagggttga gactcggg                               18
283 <210> SEQ ID NO: 13
284 <211> LENGTH: 18
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Antisense Oligonucleotide
291 <400> SEQUENCE: 13
292   acagttgagg gttgagac                               18
294 <210> SEQ ID NO: 14
295 <211> LENGTH: 18
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Antisense Oligonucleotide
302 <400> SEQUENCE: 14
303   ggtgacagtt gaggggtg                               18
305 <210> SEQ ID NO: 15
306 <211> LENGTH: 18
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Antisense Oligonucleotide
313 <400> SEQUENCE: 15
314   gcagtggtgc agcggcag                               18
316 <210> SEQ ID NO: 16
317 <211> LENGTH: 18
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Antisense Oligonucleotide
324 <400> SEQUENCE: 16
325   agggcagtgt ggcagcgg                               18
327 <210> SEQ ID NO: 17

```

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 11/09/2000
PATENT APPLICATION: US/09/695,451 TIME: 11:54:57

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11092000\I695451.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1207 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 92
L:1229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:93
L:1229 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:93
L:1230 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:93
M:340 Repeated in SeqNo=93
L:1233 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:93
L:1234 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:93
L:1237 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:93